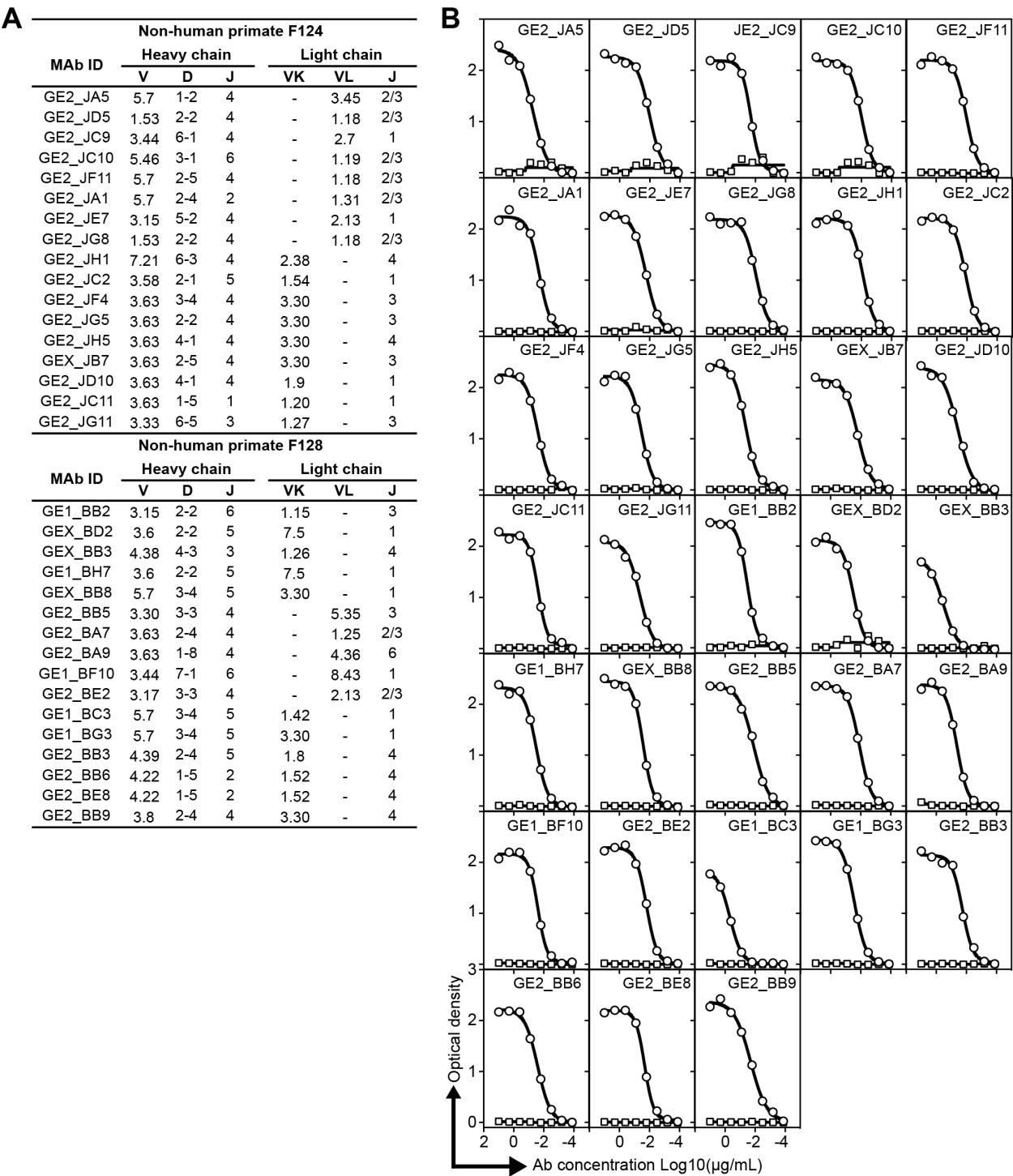


Supplementary Materials:

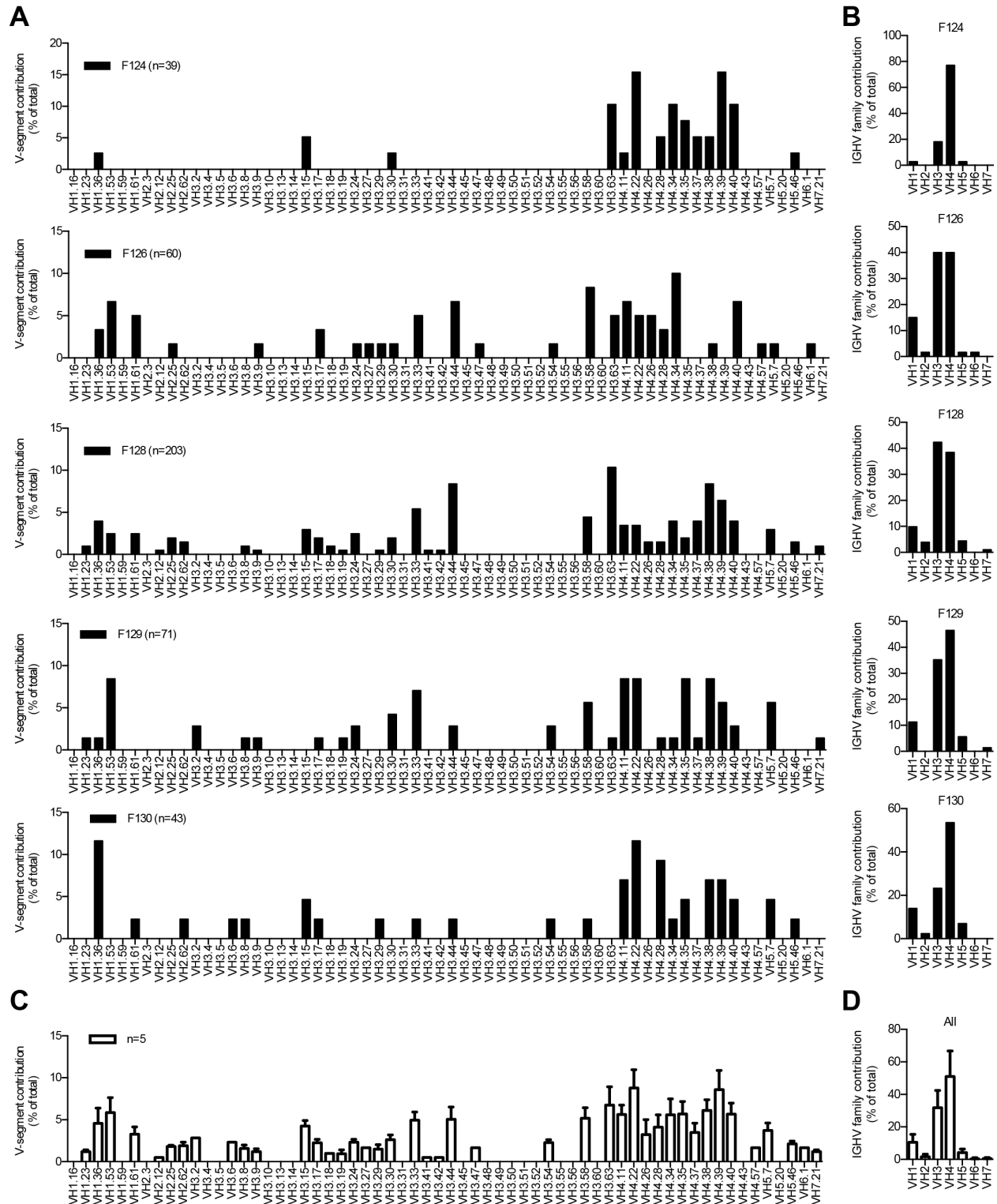
Fig. S1



**Fig. S1.** Isolated monoclonal antibody genetics and binding specificity. (A) The MAbs isolated from NHPs F124 (n=17) and F128 (n=16) are shown. Heavy chain V and light chain V and J

annotations are based on ClustalW2 alignment to a previously published rhesus macaque germline database (11, 14). Heavy chain D and J annotations are performed by IMGT®/V-Quest using the rhesus macaque option. **(B)** The MAbs were tested for specificity by ELISA. Plates were coated with similarly produced recombinant HIV-1 Env trimers (gp140-F isolate YU2; Open circles) or Influenza HA1 monomers (isolate A/Brisbane59/2007(H1N1); Open boxes). The MAb ID is shown in the individual graphs. The Y-axis indicate optical density and the X-axis indicate Ab concentration in  $\text{Log}_{10}(\mu\text{g/mL})$ .

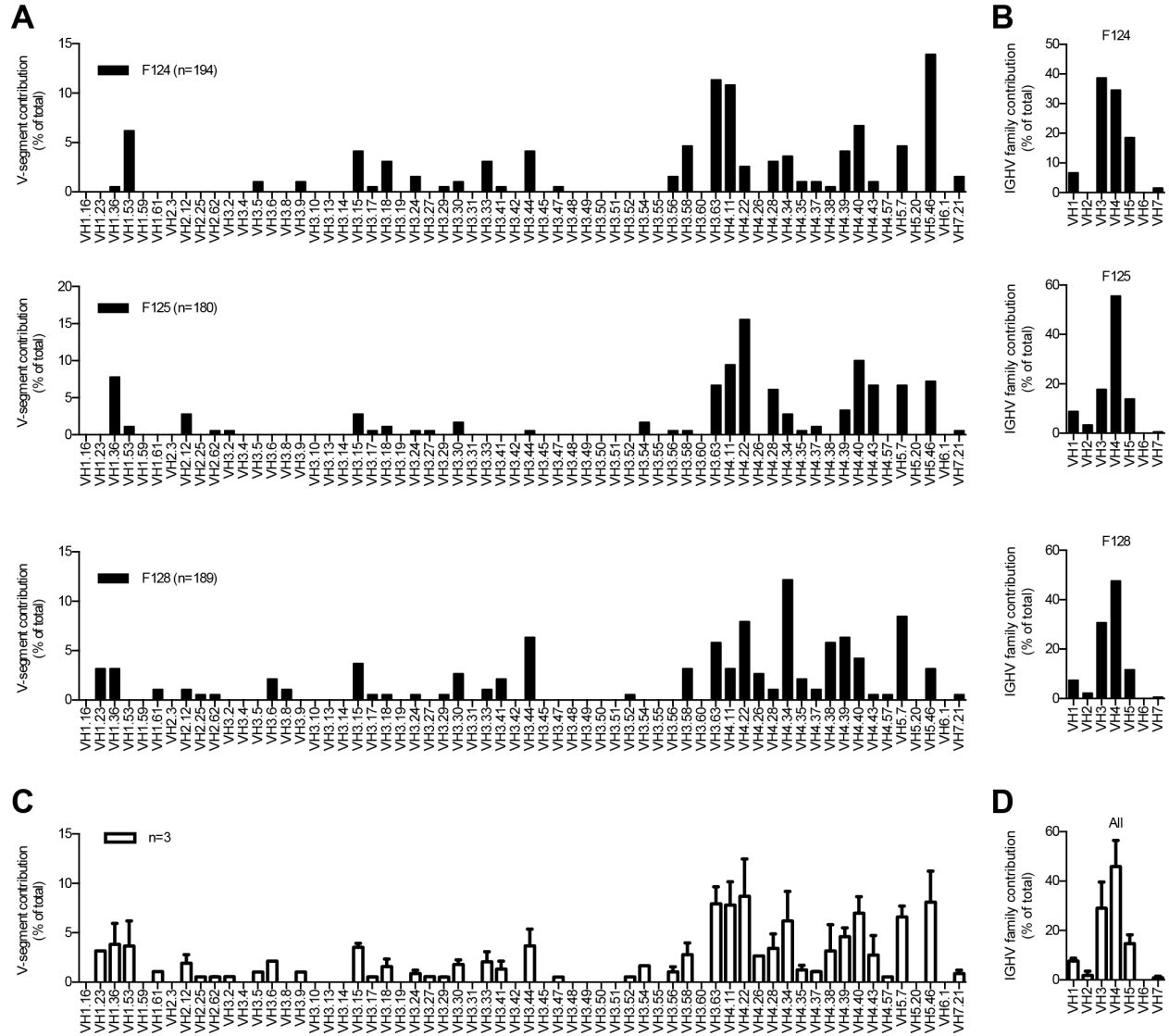
**Fig. S2**



**Fig. S2.** *V*-gene segment contribution of single sorted total memory *B* cells from individual donors. (A) Individual *V*-gene segment contribution to the total number of sequences (percent of total) for sorted total memory *B* cells (CD20<sup>+</sup>CD27<sup>+</sup>IgG<sup>+</sup>) in individual rhesus macaques. The

number of sequences (n) isolated from each donor and donor identity is indicated in the graph. **(B)** V-gene family contribution to the total number of sequences (percent of total) for each donor. **(C)** The individual V-gene segment contribution (percent of total) from each donor is merged and presented as mean +SEM (n=5). **(D)** The V-gene family contribution (percent of total) from each donor is merged and presented as mean +SEM (n=5).

**Fig. S3**



**Fig. S3.** *V*-gene segment contribution of single sorted Env-specific memory B cells from individual donors. **(A)** Individual V-gene segment contribution to the total number of sequences (percent of total) for sorted Env-specific memory B cells (CD20<sup>+</sup>CD27<sup>+</sup>IgG<sup>+</sup>gp140-F<sup>+</sup>) in individual donors. The number of sequences (n) isolated from each donor and donor identity is indicated in the graph. **(B)** V-gene family contribution to the total number of sequences (percent of total) for each donor. **(C)** The individual V-gene segment contribution (percent of total) from each donor is merged and presented as mean + SEM (n=3). **(D)** The V-gene family contribution (percent of total) from each donor is merged and presented as mean + SEM (n=3).

**Table S1.****Primers for 454-pyrosequencing library preparation**

Primer name	Sequence <sup>a</sup>	Source
<b>5' - VH1</b>		
XLR-A_VH1 LEADER-A	CCATCTCATCCCTGCGTGTCTCCGACTCAG ATGGACTGGACCTGGAGGAT	[1]
XLR-A_VH1-LEADER-F	CCATCTCATCCCTGCGTGTCTCCGACTCAG ATGGACTGGATTTGGAGGAT	[1]
XLR-A_VH1-LEADER-H_NHP	CCATCTCATCCCTGCGTGTCTCCGACTCAG TGGCAGCAGCTACAG GTGC	New design
XLR-A_VH1-LEADER-I_NHP	CCATCTCATCCCTGCGTGTCTCCGACTCAG TGACAGCAGCTACAG GCGC	New design
XLR-A_VH1-LEADER-J_NHP	CCATCTCATCCCTGCGTGTCTCCGACTCAG TGGCAGCAGCAACAG GCAC	New design
<b>5' - VH4</b>		
XLR-A_VH4 LEADER-E_NHP	CCATCTCATCCCTGCGTGTCTCCGACTCAG AGCTCCCAGATGGGTCTGTCC	New design
XLR-A_VH4 LEADER-F_NHP	CCATCTCATCCCTGCGTGTCTCCGACTCAG AGCTCCCAGATGGGTCTGTCC	New design
<b>5' - VH3</b>		
XLR-A_VH3 LEADER-A	CCATCTCATCCCTGCGTGTCTCCGACTCAG TAAAAGGTGTCCAGTGT	[1]
XLR-A_VH3 LEADER-B	CCATCTCATCCCTGCGTGTCTCCGACTCAG TAAGAGGTGTCCAGTGT	[1]
XLR-A_VH3 LEADER-C	CCATCTCATCCCTGCGTGTCTCCGACTCAG TAGAAGGTGTCCAGTGT	[1]
XLR-A_VH3 LEADER-G_NHP	CCATCTCATCCCTGCGTGTCTCCGACTCAG GGAGAGGTGTCCAGTGT	New design
XLR-A_VH3 LEADER-H_NHP	CCATCTCATCCCTGCGTGTCTCCGACTCAG TAAAAGGTGTGCAGTGT	New design
<b>3' - IgG</b>		
XLR-B_3'IgG(INTERNAL)-NHP	CCTATCCCCTGTGTGCCTTGGCAGTCTCAG GTTCAGGGAAGTAGTCCTTGAC	New design

<sup>a</sup>The sequence before the space corresponds to the adaptor tag.

[1] Scheid, J. F., *et al.* Sequence and structural convergence of broad and potent HIV antibodies that mimic CD4 binding. *Science* **333**, 1633-1637 (2011).